

SEQUENCES OF
PROTEINS OF
IMMUNOLOGICAL
INTEREST

VOLUME

FIFTH EDITION

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In Fig. 1 and in the stereomodels of antibody combining sites, the location of the allotypic regions may clearly be seen to be on the outside of V_H away from the combining site. Residues 9 and 65 of V_H are numbered and will facilitate location of the V_H allotypes. The few cDNA sequences available in 1984 (65) provided no evidence that germ line sequences encoding latent allotypes may exist in some rabbits. Since then, additional germline and expressed V_H sequences (63-65, 188, 204-206) have further refined the information on V_H allotypes and V_H sequences. Newer analyses of germline V_H genes of rabbits have provided examples of potential genes and pseudogenes which could generate latent allotype sequences by somatic gene conversion mechanisms (187, 199, 203-208). Antisera to rabbit V_H allotypes crossreact with human IgG, various other species of IgM and IgG, and with the Galapagos shark 7S immunoglobulin and correlate with the N-terminal amino acid sequence (209, 210).

It is becoming of great importance, with all of the different mechanisms which are clearly generating diversity, to evaluate the extent to which each type of diversity, other than those resulting in pseudogenes, contributes noise rather than functional differences in complementarity of antibody combining sites (70, 211).

Ohno et al. (212, 213) have proposed that the genes coding for variable domains of the light and heavy chains arose from tandem repeats of a primordial nucleotide sequence about 48 base pairs in length which subsequently diverged by mutations and deletions producing a resemblance to FR1, FR2, and FR3. The complementary strand of the primordial 48 base pair repeat of V_L became the primordial V_H . The finding (147) that the complementary strands of the human D2 and D4 minigenes coded for a portion of CDR1 of V_L tends to support this hypothesis. A 45 base pair primordial building block has also been proposed for the gene for the class I major histocompatibility complex (214).

The format of our precursor, V-region, C region sequences etc. of antibodies and T cell receptors has proven very useful in selecting primers for the polymerase chain reaction (215-217).

Constant Region Sequences

The constant region sequences were aligned in such a manner as to permit various comparisons of the light chain (C_L) and the individual domains of the heavy chain (C_H1 , C_H2 , C_H3 , and C_H4). This was accomplished by sequential numbering on the left with gaps inserted for alignment. The following numbering system is used:

108 to 215 of C_L ;
114 to 223 of C_H1 , plus the first part of hinge (224 to 241),
the end of hinge (242 and 243), and the
first two residues of CH2 (244 and 245);
246 to 360 of C_H2 ;
361 to 496 of C_H3 ;
497 to 628 of C_H4 .

The gene quadruplication in the human IgG3 hinge region (218) is numbered differently using letters 241A to 241Z, and 241AA to 241SS, and these residues should not be used in aligning domains for homology. The next two columns in the heavy chain tables indicate the EU (67) and OU (219) residue numbers, respectively. The succeeding columns which are numbered give the sequence data. The C_H and hinge domains conform to the findings of Sakano et al. (220), who defined each domain precisely by sequencing the coding and intervening nucleotide sequences bordering each domain.

The extensive nucleotide sequence data on exons for the constant regions of heavy chains have provided exact boundaries for C_H1 , hinge, C_H2 , C_H3 , and C_H4 . Usually the introns separating these domains fall within the codon for a single amino acid. We have included that amino acid residue with the domain, the exon of which contains two of the three coding nucleotides. The constant regions

EU INDEX	OU INDEX	INVARIENT RESIDUES	1 HUMAN IGM'CL	2 HUMAN IGM'CL	3 GAL OU	4 BOT	5 X17115 CL	6 GLI	7 HUMAN IGM MEMB'CL	8 NIG	9 ER1	10 HUMAN IGD'CL	11 HUMAN IGD'CL	12 HUMAN IGD'CL	13 HUMAN IGD'CL	14 HUMAN IGD'CL	15 OMH	16 HERA	17 FRO	18 JON	19 WIS
243A		VAL	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243B		SER	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243C		THR	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243D		PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243E		PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243F		PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243G	230	VAL	VAL	VAL	VAL	VAL	VAL	VAL	---	---	---	---	---	---	---	---	---	---	---	---	---
243H	231	ILE	ILE	ILE	ILE	ILE	ILE	ILE	---	---	---	---	---	---	---	---	---	---	---	---	---
243I	232	ALA	ALA	ALA	ALA	ALA	ALA	ALA	---	---	---	---	---	---	---	ALA	ALA	ALA	ALA	ALA	ALA
244	231	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
245	232	---	---	---	---	---	---	---	---	---	---	---	---	---	---	PRO	PRO	PRO	PRO	PRO	PRO
245A		PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
245B		PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
245C		GLU	GLU	GLX	GLU	GLU	GLU	GLU	SER	SER	SER	SER	SER	SER	SER	GLU	GLU	GLU	GLU	GLU	GLU
246	233	LEU	LEU	LEU	LEU	LEU	LEU	LEU	HIS	HIS	HIS	HIS	HIS	HIS	HIS	LEU	LEU	LEU	LEU	LEU	LEU
247	234	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	LEU	LEU	LEU	LEU	LEU	LEU
248	235	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
249	236	LYS	LYS	LYS	LYS	LYS	LYS	LYS	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLY	GLY	GLY	GLY	GLY	GLY
250	237	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LEU	LEU	LEU	LEU	LEU	LEU	LEU	PRO	PRO	PRO	PRO	PRO	PRO
251	238	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
251A		CYS	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
251B		SER	SER	SER	SER	SER	SER	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	SER	SER	SER	SER	SER	SER
252	239	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	SER	SER	SER	SER	SER	SER
253	240	PHE	PHE	PHE	PHE	PHE	PHE	PHE	TYR	TYR	TYR	TYR	TYR	TYR	TYR	VAL	VAL	VAL	VAL	VAL	VAL
254	241	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
255	242	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
256	243	---	---	---	---	---	---	---	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
257	244	PRO	PRO	PRO	PRO	PRO	PRO	PRO	THR	THR	THR	THR	THR	THR	THR	PHE	PHE	PHE	PHE	PHE	PHE
258	245	ARG	ARG	ARG	ARG	ARG	ARG	ARG	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
259	246	---	---	---	---	---	---	---	ALA	ALA	ALA	ALA	ALA	ALA	ALA	LYS	LYS	LYS	LYS	LYS	LYS
260	247	ASP	ASP	ASP	ASP	ASP	ASP	ASP	GLN	GLN	GLN	GLN	GLN	GLN	GLN	PRO	PRO	PRO	PRO	PRO	PRO
261	248	GLY	GLY	GLY	GLY	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LYS	LYS	LYS	LYS	LYS	LYS
262	249	PHE	PHE	PHE	PHE	PHE	PHE	PHE	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ARG	ARG	ARG	ARG	ARG	ARG
263	250	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
264	251	PHE	PHE	PHE	PHE	PHE	PHE	PHE	LEU	LEU	LEU	LEU	LEU	LEU	LEU	THR	THR	THR	THR	THR	THR
265	252	---	---	---	---	---	---	---	TRP	TRP	TRP	TRP	TRP	TRP	TRP	MET	MET	MET	MET	MET	MET
266	253	GLN	GLN	GLN	GLN	GLN	GLN	GLN	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ILE	ILE	ILE	ILE	ILE	ILE
267	254	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ARG	ARG	ARG	ARG	ARG	ARG	ARG	SER	SER	SER	SER	SER	SER
268	255	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ASP	ASP	ASP	ASP	ASP	ASP	ASP	SER	SER	SER	SER	SER	SER
269	256	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	ARG	ARG	ARG	ARG	ARG	ARG
270	257	SER	SER	SER	SER	SER	SER	SER	ALA	ALA	ALA	ALA	ALA	ALA	ALA	PRO	PRO	PRO	PRO	PRO	PRO
271	258	LYS	LYS	LYS	LYS	LYS	LYS	LYS	GLU	GLU	GLU	GLU	GLU	GLU	GLU	PRO	PRO	PRO	PRO	PRO	PRO
272	259	LEU	LEU	LEU	LEU	LEU	LEU	LEU	PHE	PHE	PHE	PHE	PHE	PHE	PHE	VAL	VAL	VAL	VAL	VAL	VAL
273	260	ILE	ILE	ILE	ILE	ILE	ILE	ILE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
274	261	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
275	262	GLN	GLN	GLN	GLN	GLN	GLN	GLN	PHE	PHE	PHE	PHE	PHE	PHE	PHE	VAL	VAL	VAL	VAL	VAL	VAL
276	263	ALA	ALA	ALA	ALA	ALA	ALA	ALA	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
277	264	THR	THR	THR	THR	THR	THR	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	VAL
278	265	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ASP	ASP	ASP	ASP	ASP	ASP
279	266	PHE	PHE	PHE	PHE	PHE	PHE	PHE	SER	SER	SER	SER	SER	SER	SER	VAL	VAL	VAL	VAL	VAL	VAL
280	267	SER	SER	SER	SER	SER	SER	SER	ASP	ASP	ASP	ASP	ASP	ASP	ASP	SER	SER	SER	SER	SER	SER
281	268	PRO	PRO	PRO	PRO	PRO	PRO	PRO	LEU	LEU	LEU	LEU	LEU	LEU	LEU	HIS	HIS	HIS	HIS	HIS	HIS
282	269	ARG	ARG	ARG	ARG	ARG	ARG	ARG	LYS	LYS	LYS	LYS	LYS	LYS	LYS	GLU	GLU	GLU	GLU	GLU	GLU
283	270	GLN	GLN	GLN	GLN	GLN	GLN	GLN	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
284	271	ILE	ILE	ILE	ILE	ILE	ILE	ILE	PRO	PRO	PRO	PRO	PRO	PRO	PRO	---	---	---	---	---	---
285	272	GLN	GLN	GLN	---	GLU	GLN	GLN	ALA	ALA	ALA	ALA	ALA	ALA	ALA	GLU	GLU	GLU	GLU	GLU	GLU
286	273	VAL	VAL	VAL	VAL	VAL	VAL	VAL	---	---	---	---	---	---	---	---	VAL	VAL	VAL	VAL	VAL
287	274	---	---	---	---	---	---	---	HIS	HIS	HIS	HIS	HIS	HIS	HIS	GLN	GLN	GLN	GLN	GLN	GLN
288	275	SER	SER	SER	TRP	SER	SER	SER	LEU	LEU	LEU	LEU	LEU	LEU	LEU	PHE	PHE	PHE	PHE	PHE	PHE
289	276	---	---	---	---	---	---	---	THR	THR	THR	THR	THR	THR	THR	LYS	LYS	LYS	LYS	LYS	LYS
290	277	TRP	TRP	TRP	SER	TRP	TRP	TRP	GLU	GLU	GLU	GLU	GLU	GLU	GLU	TRP	TRP	TRP	TRP	TRP	TRP
291	278	LEU	LEU	LEU	ARG	ARG	ARG	ARG	VAL	VAL	VAL	VAL	VAL	VAL	VAL	TYR	TYR	TYR	TYR	TYR	TYR
292	279	GLY	GLY	GLY	GLY	GLY	GLY	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
293	280	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	---	---	---	---	---	---	---	---	---	---	---	---
294	281	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
295	282	LYS	LYS	LYS	LYS	LYS	LYS	LYS	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ASP	ASP	ASP	ASP	ASP	ASP
296	283	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
297	284	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LYS	LYS	LYS	LYS	LYS	LYS	LYS	---	---	---	---	---	---
298	285	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	---	---	---	---	---	---	---	---	---	---	---	---
299	286	SER	SER	SER	SER	SER	SER	SER	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
300	287	GLY	GLY	GLY	GLY	GLY	GLY	GLY	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLU	GLU	GLU	GLU	GLU	GLU
301	288	VAL	VAL	VAL	VAL	VAL	VAL	VAL	THR	THR	THR	THR	THR	THR	THR	VAL	VAL	VAL	VAL	VAL	VAL
302	289	THR	THR	THR	THR	THR	THR	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	HIS	HIS	HIS	HIS	HIS	HIS
303	290	---	---	---	---	---	---	---	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ASN	ASN	ASN	ASN	ASN	ASN
304	291	THR	THR	THR	THR	THR	THR	THR	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ALA	ALA	ALA	ALA	ALA	ALA
305	292	ASP	ASP	ASN	ASN	ASN	ASN	ASN	GLU	GLU	GLU	GLU	GLU	GLU	GLU	LYS	LYS	LYS	LYS	LYS	LYS
306	293	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLU	GLU	GLU	GLU	GLU	GLU	GLU	THR	THR	THR	THR	THR	THR
307	294	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	PRO	PRO	PRO	PRO	PRO	PRO
308	295	GLN	GLN	GLN	GLN	GLN	GLN	GLN	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ARG	ARG	ARG	ARG	ARG	ARG
309	296	ALA	ALA	ALA	ALA	ALA	ALA	ALA	LEU	LEU	LEU	LEU	LEU	LEU	LEU	ARG	ARG	ARG	ARG	ARG	ARG
310	297	GLU	GLU	GLX	GLX	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
311	298	ALA	ALA	ALA	ALA	ALA	ALA	ALA	HIS	HIS	HIS	HIS	HIS	HIS	HIS	GLN	GLN	GLN	GLN	GLN	GLN
312	299	LYS	LYS	LYS	LYS	LYS	LYS	LYS	---	---	---	---	---	---	---	TYR	TYR	TYR	TYR	TYR	TYR
313	300	GLU	GLU	GLX	GLX	GLU	GLU	GLU	---	---	---	---	---	---	---	---	---	---	---	---	---
314	301	SER	SER	SER	SER	SER	SER	SER	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
315	302	GLY	GLY	GLY	GLY	GLY	GLY	GLY	---	---	---	---	---	---	---	---	---	---	---	---	---
316	303	PRO	PRO	PRO	PRO	PRO	PRO	PRO	---	---	---	---	---								

EU INDEX	OU INDEX	20 SPA	21 ZUC	22 ZUC	23 KUP	24 BRU	25 JTR	26 CHA	27 GOE	28 EU	29 NE	30 CRA	31 VAU	32 LEB	33 EST	34 YOK	35 SAC	36 HUMAN	37 KOL	38 MCG	39 LEC	40 DOB	41 BUR	42 TRO	43 CAR	
243A																										
243B																										
243C																										
243D																										
243E																										
243F																										
243G																										
243H																										
243I																										
244	231		ALA	ALA	ALA	ALA		ALA	ALA	ALA						ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA	
245	232		PRO	PRO	PRO	PRO		PRO	PRO	PRO						PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	
245A																										
245B																										
245C																										
246	233	233	GLU	GLU	GLU	GLU		GLU	GLU	GLN						GLU	GLU	GLU	GLX	GLU	GLU	GLU	GLU	GLU	GLU	
247	234	234	LEU	LEU	LEU	LEU		LEU	LEU	LEU						LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
248	235	235	LEU	LEU	LEU	LEU		LEU	LEU	LEU						LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
249	236	236	GLY	GLY	GLY	GLY		GLY	GLY	GLY						GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
250	237	237	GLY	GLY	GLY	GLY		GLY	GLY	GLY						GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
251	238	238	PRO	PRO	PRO	PRO		PRO	PRO	PRO						PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
251A																										
251B																										
252	239	239	SER	SER	SER	SER		SER	SER	SER						SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
253	240	240	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
254	241	241	PHE	PHE	PHE	PHE		PHE	PHE	PHE						PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	
255	242	242	LEU	LEU	LEU	LEU		LEU	LEU	LEU						LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
256	243	243	PHE	PHE	PHE	PHE		PHE	PHE	PHE						PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	
257	244	243	PRO	PRO	PRO	PRO		PRO	PRO	PRO						PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
258	245	244	PRO	PRO	PRO	PRO		PRO	PRO	PRO						PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
259	246	245	LYS	LYS	LYS	LYS		LYS	LYS	LYS						LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
260	247	246	PRO	PRO	PRO	PRO		PRO	PRO	PRO						PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
261	248	247	LYS	LYS	LYS	LYS		LYS	LYS	LYS						LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
262	249	248	ASP	ASP	ASP	ASP		ASP	ASP	ASP						ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
263	250	249	THR	THR	THR	THR		THR	THR	THR						THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
264	251	249	LEU	LEU	LEU	LEU		LEU	LEU	LEU						LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
265	252	250	MET	MET	MET	MET		MET	MET	MET						MET	MET	MET	MET	MET	MET	MET	MET	MET	MET	
266	253	251	ILE	ILE	ILE	ILE		ILE	ILE	ILE						ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	
267	254	252	SER	SER	SER	SER		SER	SER	SER						SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
268	255	253	ARG	ARG	ARG	ARG		ARG	ARG	ARG						ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	
269	256	254	THR	THR	THR	THR		THR	THR	THR						THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
270	257	255	PRO	PRO	PRO	PRO		PRO	PRO	PRO						PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
271	258	256	GLU	GLU	GLU	GLU		GLU	GLU	GLU						GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	
272	259	257	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
273	260	258	THR	THR	THR	THR		THR	THR	THR						THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
274	261	259	CYS	CYS	CYS	CYS		CYS	CYS	CYS						CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	
275	262	260	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
276	263	261	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
277	264	262	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
278	265	263	ASP	ASP	ASP	ASP		ASP	ASP	ASP						ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
279	266	264	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
280	267	265	SER	SER	SER	SER		SER	SER	SER						SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
281	268	266	HIS	HIS	HIS	HIS		HIS	HIS	HIS						SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
282	269	267	GLU	GLU	GLU	GLU		GLU	GLU	GLU						HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	
283	270	268	ASP	ASP	ASP	ASP		ASP	ASP	ASP						ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
284	271	269	PRO	PRO	PRO	PRO		PRO	PRO	PRO						PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
285	272	270	GLX	GLX	GLX	GLX		GLX	GLX	GLX						GLX	GLX	GLX	GLX	GLX	GLX	GLX	GLX	GLX	GLX	
286	273	271	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
287	274	272	GLX	GLX	GLX	GLX		GLX	GLX	GLX						GLX	GLX	GLX	GLX	GLX	GLX	GLX	GLX	GLX	GLX	
288	275	273	PHE	PHE	PHE	PHE		PHE	PHE	PHE						PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	
289	276	274	LYS	LYS	LYS	LYS		LYS	LYS	LYS						LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
290	277	275	TYR	TYR	TYR	TYR		TYR	TYR	TYR						TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	
291	278	276	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
292	279	277	---	---	---	---		---	---	---						---	---	---	---	---	---	---	---	---	---	---
293	280	278	ASP	ASP	ASP	ASP		ASP	ASP	ASP						ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
294	281	279	GLY	GLY	GLY	GLY		GLY	GLY	GLY						GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
295	282	280	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
296	283	281	GLN	GLN	GLN	GLN		GLN	GLN	GLN						GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	
297	284	282	VAL	VAL	VAL	VAL		VAL	VAL	VAL						VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
298	285	283	HIS	HIS	HIS	HIS		HIS	HIS	HIS						HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	
299	286	284	ASN	ASN	ASN	ASN		ASN	ASN	ASN						ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	
300	287	285	ALA	ALA	ALA	ALA		ALA	ALA	ALA						ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	
301	288	286	LYS	LYS	LYS	LYS		LYS	LYS	LYS						LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
302	289	287	THR	THR	THR	THR		THR	THR	THR						THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
303	290	288	LYS	LYS	LYS	LYS		LYS	LYS	LYS						LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	
304	291	289	PRO	PRO	PRO	PRO		PRO	PRO	PRO						PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	
305	292	290	ARG	ARG	ARG	ARG		ARG	ARG	ARG						ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	
306	293	291	GLX	GLX	GLX	GLX		GLX	GLX	GLX						GLX	GLX	GLX	GLX	GLX	GLX	GLX	GLX	GLX	GLX	
307	294	292	GLN	GLN	GLN	GLN		GLN	GLN	GLN						GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	
308	295	293	GLX	GLX	GLX	GLX		GLX	GLX	GLX						GLX	GLX	GLX	GLX	GLX						

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

EU INDEX	OU INDEX	44 CHIMPAN- ZEE CH4-14 (IGG1) 'CL	45 HUMAN IGA1 'CL	46 GORILLA IGA1 'CL	47 HUMAN IGG 'CL	48 HUMAN IGG2 'CL	49 TIL	50 ZIE	51 SA	52 FIG	53 HUMAN IGG4 'CL	54 VIN	55 HUMAN IGE 'CL	56 HUMAN IGE 'CL	57 CHIMP IGE 'CL	58 ORAN- GUTAN IGE 'CL	59 U266 'CL	60 ND	61 BUT	62 LAN
243A		---	VAL	VAL	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243B		---	PRO	PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243C		---	SER	SER	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243D		---	THR	THR	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243E		---	PRO	PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243F		---	PRO	PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
243G	230	---	THR	THR	---	---	---	---	---	---	---	---	VAL	---	VAL	VAL	VAL	VAL	---	---
243H	231	---	PRO	PRO	---	---	---	---	---	---	---	---	CYS	---	CYS	CYS	CYS	CYS	---	---
243I	232	---	SER	SER	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
244	231	ALA	PRO	PRO	THR	ALA	ALA	ALA	ALA	ALA	ALA	ALA	---	---	---	---	---	---	---	---
245	232	PRO	SER	SER	THR	PRO	PRO	---	---	---	---	---	---	---	---	---	---	---	---	---
245A		---	THR	THR	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
245B		---	PRO	PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
245C		---	PRO	PRO	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
246	233	233	GLU	THR	THR	GLU	PRO	PRO	---	---	---	---	ARG	---	ARG	ARG	ARG	ARG	VAL	VAL
247	234	234	LEU	PRO	PRO	PRO	VAL	VAL	---	---	---	PHE	PHE	ASP	---	ASP	ASP	ASP	PRO	PRO
248	235	235	LEU	SER	SER	LEU	ALA	ALA	---	---	---	LEU	LEU	PHE	---	PHE	PHE	PHE	PRO	PRO
249	236	236	PRO	PRO	PRO	GLY	---	---	---	---	---	GLY	GLY	THR	---	THR	THR	THR	PRO	PRO
250	237	237	GLY	SER	PRO	GLY	---	---	---	---	---	---	---	---	---	---	---	---	---	---
251	238	238	PRO	CYS	CYS	PRO	PRO	PRO	---	---	---	PRO	PRO	PRO	PRO	PRO	PRO	PRO	CYS	CYS
251A		---	---	CYS	CYS	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
251B		---	HIS	HIS	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
252	239	239	SER	PRO	PRO	SER	SER	SER	---	---	---	SER	SER	THR	THR	THR	THR	THR	PRO	PRO
253	240	240	VAL	ARG	ARG	VAL	VAL	VAL	---	---	---	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ARG	ARG
254	241	241	PHE	LEU	LEU	PHE	PHE	PHE	---	---	---	PHE	PHE	LYS	LYS	LYS	LYS	LYS	LEU	LEU
255	242	242	LEU	SER	SER	LEU	LEU	LEU	---	---	---	LEU	LEU	ILE	ILE	ILE	ILE	ILE	SER	SER
256	243	243	ASP	LEU	LEU	PHE	PHE	ASP	---	---	---	PHE	PHE	LEU	LEU	LEU	LEU	LEU	LEU	LEU
257	244	243	PRO	HIS	HIS	PRO	PRO	PRO	---	---	---	GLN	GLN	GLN	GLN	GLN	GLN	GLN	PRO	PRO
258	245	244	PRO	ARG	ARG	PRO	PRO	PRO	---	---	---	PRO	PRO	SER	SER	SER	SER	SER	ARG	ARG
259	246	245	LYS	PRO	PRO	LYS	LYS	LYS	---	---	---	LYS	LYS	SER	SER	SER	SER	SER	PRO	PRO
260	247	246	PRO	ALA	ALA	PRO	PRO	PRO	---	---	---	PRO	PRO	CYS	CYS	CYS	CYS	CYS	ALA	ALA
261	248	247	LYS	LEU	LEU	LYS	LYS	LYS	---	---	---	LYS	LYS	ASP	ASP	ASP	ASP	ASP	LEU	LEU
262	249	248	ASP	GLU	GLU	ASP	ASP	ASP	---	---	---	ASP	ASP	GLY	GLY	GLY	GLY	GLY	GLU	GLU
263	250	249	THR	THR	THR	THR	THR	THR	---	---	---	THR	THR	GLY	GLY	GLY	GLY	GLY	ASP	ASP
264	251	249	LEU	LEU	LEU	LEU	LEU	LEU	---	---	---	LEU	LEU	GLY	GLY	GLY	GLY	GLY	LEU	LEU
265	252	250	MET	LEU	LEU	MET	MET	MET	---	---	---	MET	MET	HIS	HIS	HIS	HIS	HIS	LEU	LEU
266	253	251	ILE	LEU	LEU	ILE	ILE	ILE	---	---	---	ILE	ILE	PHE	PHE	PHE	PHE	PHE	LEU	LEU
267	254	252	SER	GLY	GLY	SER	SER	SER	---	---	---	SER	SER	PRO	PRO	PRO	PRO	PRO	GLY	GLY
268	255	253	ARG	SER	SER	ARG	ARG	ARG	---	---	---	ARG	ARG	PRO	PRO	PRO	PRO	PRO	SER	SER
269	256	254	THR	GLU	GLU	THR	THR	THR	---	---	---	THR	THR	THR	THR	THR	THR	THR	GLU	GLU
270	257	255	PRO	ALA	ALA	PRO	PRO	PRO	---	---	---	PRO	PRO	ILE	ILE	ILE	ILE	ILE	ALA	ALA
271	258	256	GLU	ASN	ASN	GLU	GLU	GLU	---	---	---	GLU	GLU	GLN	GLN	GLN	GLN	GLN	ASN	ASN
272	259	257	VAL	VAL	VAL	VAL	VAL	VAL	---	---	---	VAL	VAL	LEU	LEU	LEU	LEU	LEU	THR	THR
273	260	258	THR	THR	THR	THR	THR	THR	---	---	---	THR	THR	LEU	LEU	LEU	LEU	LEU	THR	THR
274	261	259	CYS	CYS	CYS	CYS	CYS	CYS	---	---	---	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
275	262	260	VAL	THR	THR	VAL	VAL	VAL	---	---	---	VAL	VAL	LEU	LEU	LEU	LEU	LEU	THR	THR
276	263	261	VAL	LEU	LEU	VAL	VAL	VAL	---	---	---	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LEU	LEU
277	264	262	VAL	THR	THR	VAL	VAL	VAL	---	---	---	VAL	VAL	SER	SER	SER	SER	SER	THR	THR
278	265	263	GLY	ASP	ASP	GLY	GLY	GLY	---	---	---	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
279	266	264	VAL	LEU	LEU	VAL	VAL	VAL	---	---	---	VAL	VAL	TYR	TYR	TYR	TYR	TYR	GLY	GLY
280	267	265	SER	ARG	ARG	SER	SER	SER	---	---	---	SER	SER	THR	THR	THR	THR	THR	ARG	ARG
281	268	266	HIS	ASP	ASP	HIS	HIS	HIS	---	---	---	SER	SER	GLN	GLN	GLN	GLN	GLN	ASP	ASP
282	269	267	GLU	ALA	ALA	GLU	GLU	GLU	---	---	---	GLU	GLU	---	---	---	---	---	ALA	ALA
283	270	268	ASP	SER	SER	ASP	ASP	ASP	---	---	---	ASP	ASP	---	---	---	---	---	SER	SER
284	271	269	PRO	---	---	PRO	PRO	PRO	---	---	---	PRO	PRO	PRO	PRO	PRO	PRO	PRO	---	---
285	272	270	GLU	GLY	GLY	GLU	GLU	GLU	---	---	---	GLU	GLX	GLY	GLY	GLY	GLY	GLY	GLY	GLY
286	273	271	VAL	VAL	VAL	VAL	VAL	VAL	---	---	---	VAL	VAL	THR	THR	THR	THR	THR	GLY	GLY
287	274	272	LYS	THR	THR	LYS	GLN	GLN	---	---	---	LYS	THR	THR	THR	THR	THR	THR	ALA	ALA
288	275	273	PHE	PHE	PHE	PHE	PHE	PHE	---	---	---	PHE	PHE	ILE	ILE	ILE	ILE	ILE	THR	THR
289	276	274	ASN	THR	THR	ASN	ASN	ASN	---	---	---	ASN	ASN	ILE	ILE	ILE	ILE	ILE	THR	THR
290	277	275	TRP	TRP	TRP	TRP	TRP	TRP	---	---	---	TRP	TRP	THR	THR	THR	THR	THR	TRP	TRP
291	278	276	TYR	TYR	TYR	TYR	TYR	TYR	---	---	---	TYR	TYR	THR	THR	THR	THR	THR	TRP	TRP
292	279	277	VAL	PRO	PRO	VAL	VAL	VAL	---	---	---	VAL	VAL	LEU	LEU	LEU	LEU	LEU	SER	SER
293	280	278	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
294	281	279	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
295	282	280	ASP	SER	SER	ASP	ASP	ASP	---	---	---	ASP	ASP	GLU	GLU	GLU	GLU	GLU	GLX	---
296	283	281	GLY	SER	SER	GLY	GLY	GLY	---	---	---	GLY	GLY	ASP	ASP	ASP	ASP	ASP	ASP	ASP
297	284	282	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
298	285	283	VAL	GLY	GLY	VAL	VAL	VAL	---	---	---	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY
299	286	284	GLU	LYS	LYS	GLU	GLU	GLU	---	---	---	GLU	GLU	GLN	GLN	GLN	GLN	GLN	GLX	---
300	287	285	VAL	SER	SER	VAL	VAL	VAL	---	---	---	VAL	VAL	VAL	VAL	VAL	VAL	VAL	SER	SER
301	288	286	ALA	HIS	HIS	ALA	ALA	ALA	---	---	---	ALA	ALA	MET	MET	MET	MET	MET	ALA	ALA
302	289	287	ASN	VAL	VAL	ASN	ASN	ASN	---	---	---	ASN	ASN	---	---	---	---	---	VAL	VAL
303	290	288	ALA	GLN	GLU	ALA	ALA	ALA	---	---	---	ALA	ALA	ASP	ASP	ASP	ASP	ASP	GLY	GLY
304	291	289	LYS	GLY	GLY	LYS	LYS	LYS	---	---	---	LYS	LYS	VAL	VAL	VAL	VAL	VAL	GLY	GLY
305	292	290	THR	PRO	PRO	THR	THR	THR	---	---	---	THR	THR	ASP	ASP	ASP	ASP	ASP	PRO	PRO
306	293	291	LYS	PRO	PRO	LYS	LYS	LYS	---	---	---	LYS	LYS	LEU	LEU	LEU	LEU	LEU	PRO	PRO
307	294	292	PRO	GLU	GLU	PRO	PRO	PRO	---	---	---	PRO	PRO	SER	SER	SER	SER	SER	GLU	GLU
308	295	293	ARG	ARG	ARG	ARG	ARG	ARG	---	---	---	ARG	ARG	THR	THR	THR	THR	THR	SER	SER
309	296	294	GLU	ASP	ASP	GLU	GLU	GLU	---	---	---	GLU	GLU	ALA	ALA	ALA	ALA	ALA	ASP	ASP
310	297	295	GLN	LEU	LEU	GLN	GLN	GLN	---	---	---	GLN	GLN	SER	SER	SER	SER	SER	SER	SER
311	298	296	TYR	CYS	CYS	TYR	PHE	PHE	---	---	---	PHE	PHE	THR	THR	THR	THR	THR	GLY	GLY
312	299	297	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
313	300	298	ASN	CYS	CYS	ASN	ASN	ASN	---	---	---	ASN	ASN	GLN	GLN	GLN	GLN	GLN	SER	CYS
314	301	299	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
315	302	300	GLY	---	---	GLY	---	---	---	---	---	---	---	---	---	---	---	---	---	---
316	303	301	SER	---	---	SER	SER	SER	---	---	---	SER	SER	GLY	GLY	GLY	GLY	GLY	---	---
317	304	302	THR	---	---	THR	THR	THR	---	---	---	THR	THR	LEU	LEU	LEU	LEU	LEU	---	---
318	305	303	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
319	306	304	TYR	TYR	TYR	TYR	PHE	PHE	---	---	---	TYR	TYR	ALA	ALA	ALA	ALA	ALA	TYR	TYR
320	307	305	ARG	SER	SER	ARG	ARG	ARG												

EU INDEX	OU INDEX	63 HUMAN IGA2 'CL	64 HUMAN IGA2 A2M(1) 'CL	65 HUMAN IGA2 A2M(2) 'CL	66 IGM 'CL	67 IGM 'CL	68 IGM-b 'CL	69 MUTANT 102 'CL	70 HOPC 104E	71 HOPC 104E MEMB 'CL	72 HPC76 'CL	73 G8 CA 'CL	74 GAT50 'CL	75 IGD 'CL	76 IGD SECR 'CL	77 IGD MEMB 'CL	78 B1-8 DELTA1	79 MOUSE IGG3 'CL	80 IGG3 MEMB 'CL
243A																			
243B																			
243C																			
243D																			
243E																			
243F																			
243G		230			ALA	ALA	ALA		ALA										
243H		232			ALA	ALA	ALA		ALA										
243I																			
244	231																		
245	232																		PRO
245A																			GLY
245B																			
245C																			
246	233	233			VAL	PRO													
247	234	234			GLU	GLU	GLU		GLU										ASN
248	235	235			PRO	MET	MET		MET										ILE
249	236	236			PRO	ASN	ASN		ASN										LEU
250	237	237			PRO	ASN	ASN		ASN										GLY
251	238	238			PRO	ASN	ASN		ASN										GLY
251A					CYS	VAL	VAL		VAL										PRO
251B					HIS														
252	239	239			PRO	ASN	ASN		ASN										
253	240	240			ARG	VAL	VAL		VAL										SER
254	241	241			LEU	PHE	PHE		PHE										VAL
255	242	242			SER	VAL	VAL		VAL										PHE
256	243	243			LEU														ILE
257	244	243			HIS	PRO	PRO		PRO										PHE
258	245	244			ARG	PRO	PRO		PRO										PRO
259	246	245			PRO	ARG	ARG		ARG										PRO
260	247	246			ALA	LEU	ASP		ASP										LYS
261	248	247			GLU	GLU	GLY		GLY										PRO
262	249	248			LEU	GLY	PHE		PHE										LYS
263	250	249			ASP	ASP	PHE		PHE										ASP
264	251	249			LEU	LEU	GLY		GLY										ALA
265	252	250			LEU	LEU	PRO		PRO										LEU
266	253	251			LEU	LEU	ALA		ALA										MET
267	254	252			GLY	GLY	PRO		PRO										ILE
268	255	253			SER	SER	ARG		ARG										SER
269	256	254			GLU	GLU	LYS		LYS										LEU
270	257	255			ALA	ALA	SER		SER										THR
271	258	256			ASN	ASN	LYS		LYS										PRO
272	259	257			LEU	LEU	LEU		LEU										LYS
273	260	258			THR	THR	ILE		ILE										VAL
274	261	259			CYS	CYS	CYS		CYS										THR
275	262	260			THR	THR	GLU		GLU										CYS
276	263	261			LEU	LEU	ALA		ALA										VAL
277	264	262			THR	THR	THR		THR										VAL
278	265	263			GLY	GLY	ASN		ASN										VAL
279	266	264			LEU	LEU	PHE		PHE										ASP
280	267	265			ARG	ARG	THR		THR										VAL
281	268	266			ASP	ASP	PRO		PRO										SER
282	269	267			ALA	ALA	LYS		LYS										GLU
283	270	268			SER	SER	PRO		PRO										ASP
284	271						ILE		ILE										PRO
285	272				GLY	GLY	THR		THR										ASP
286	273	269			ALA	ALA	VAL		VAL										VAL
287	274				THR	THR	THR		THR										ASP
288	275				PHE	PHE	THR		THR										VAL
289	276	270			THR	THR	SER		SER										HIS
290	277	271			TRP	TRP	TRP		TRP										SER
291	278	272			THR	THR	LEU		LEU										TRP
292	279				PRO	PRO	LYS		LYS										PHE
293		274			THR	THR	ASP		ASP										VAL
294		275			PRO	PRO	GLY		GLY										VAL
295	280	276			SER	SER	LYS		LYS										
296	281	277			SER	SER	LEU		LEU										ASP
297		278					VAL		VAL										ASN
298		279			SER	SER	GLU		GLU										
299	282	280			GLY	GLY	SER		SER										
300	283	281			LYS	LYS	GLY		GLY										LYS
301	284	282			SER	SER	PHE		PHE										GLU
302	285	283			ALA	ALA	THR		THR										VAL
303	286				VAL	VAL	THR		THR										HIS
304	287	284			GLN	GLN	THR		THR										THR
305	288	285			GLY	GLY	ASP		ASP										ALA
306	289	286			PRO	PRO	PRO		PRO										TRP
307	290	287			PRO	PRO	VAL		VAL										THR
308	291	288			GLU	GLU	THR		THR										GLN
309	292	289			ARG	ARG	ILE		ILE										PRO
310	293	290			ASP	ASP	GLU		GLU										ARG
311	294	291			LEU	LEU	ASN		ASN										GLU
312	295	292			CYS	CYS	LYS		LYS										ALA
313	296	293			GLY	GLY	GLY		GLY										GLN
314	297	294			CYS	CYS	SER		SER										TYR
315		295					THR		THR										ASN
316		296					PRO		PRO										
317	298	297					GLN		GLN										
318	299	298					THR		THR										SER
319	300	299			TYR	TYR	TYR		TYR										THR
320	301	300			SER	SER	LYS		LYS										PHE
321	302	301			VAL	VAL	VAL		VAL										ARG
322	303	302			SER	SER	VAL		VAL										VAL
323	304	303			SER	SER	ILE		ILE										VAL
324	305	304			VAL	VAL	THR		THR										SER
325	306	305			LEU	LEU	LEU		LEU										ALA
326	307	306			PRO	PRO	THR		THR										LEU
327	308	307			GLY	GLY	ILE		ILE										PRO
328	309	308			CYS	CYS	SER		SER										ILE
329	310	309			ALA	ALA	GLU		GLU										GLN
330	311	310			GLN	GLN	ILE		ILE										THR
331	312	311			PRO	PRO	ASP		ASP										HIS
332	313	312			TRP	TRP	THR		THR										ASP
333	314	313			ASN	ASN	LEU		LEU										TRP
334																			MET
335	315	314			HIS	HIS	ASN		ASN										
336	316	315			GLY	GLY	LEU		LEU										ASN
337	317	316			GLU	GLU	ASN		ASN										ARG
338	318	317			THR	THR	VAL		VAL										LYS
339	319	318			PHE	PHE	TYR		TYR										GLU
340	320	319			THR	THR	THR		THR										PHE
341	321	320			CYS	CYS	CYS		CYS										LYS
342	322	321			THR	THR	ARG		ARG										CYS
343	323	322			ALA	ALA	VAL		VAL										LYS
344	324	323			ALA	ALA	ASP		ASP										VAL
345	325	324																	

	EU INDEX	OU INDEX	81 IGG1 CL	82 IGG1 CL	83 MOPC 21	84 IF2 CL	85 ICR 11.19.3	86 IGG2B CL	87 IGG2B CL	88 IGG2B CL	89 IGG2B CL	90 MPC 11	91 10.1	92 IGG2A CL	93 17/9 CL	94 IGG2A CL	95 IGG2A CL	96 IGG2A CL	97 MOPC 173	98 CBPC 101	99 IGA 18
243A																					
243B																					
243C																					
243D																					
243E																					
243F																					
243G		230																			
243H		231																			
243I		232																			
244	231		VAL		VAL	VAL		ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
245	232		PRO		PRO	PRO		PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
245A																					
245B																					
245C																					
246	233	233						ASN	ASN	ASN		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
247	234	234						LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
248	235	235						GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
249	236	236						GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
250	237	237						PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
251	238	238																			
251A																					
251B																					
252	239	239	SER		SER	SER		SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
253	240	240	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
254	241	241	PHE		PHE	PHE		PHE	PHE	PHE		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
255	242	242	ILE		ILE	ILE		ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
256	243	243	PRO		PRO	PRO		PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
257	244	243	PRO		PRO	PRO		PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
258	245	244	PRO		PRO	PRO		PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
259	246	245	LYS		LYS	LYS		ASN	ASN	ASN		ASN	ASN	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
260	247	246	PRO		PRO	PRO		LYS	LYS	LYS		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
261	248	247	LYS		LYS	LYS		ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
262	249	248	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
263	250	249	LEU		LEU	LEU		LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
264	251	249	THR		THR	THR		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
265	252	250	THR		THR	THR		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
266	253	251	ILE		ILE	ILE		ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
267	254	252	THR		THR	THR		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
268	255	253	THR		THR	THR		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
269	256	254	THR		THR	THR		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
270	257	255	PRO		PRO	PRO		PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
271	258	256	LYS		LYS	LYS		LYS	LYS	LYS		LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS
272	259	257	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
273	260	258	THR		THR	THR		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
274	261	259	CYS		CYS	CYS		CYS	CYS	CYS		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
275	262	260	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
276	263	261	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
277	264	262	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
278	265	263	ASP		ASP	ASP		ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
279	266	264	ILE		ILE	ILE		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
280	267	265	SER		SER	SER		SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
281	268	266	LYS		LYS	LYS		GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
282	269	267	ASP		ASP	ASP		ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
283	270	268	PRO		PRO	PRO		PRO	PRO	PRO		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
284	271																				
285	272		GLU		GLU	GLU		ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
286	273	269	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
287	274		GLN		GLN	GLN		GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
288	275		PHE		PHE	PHE		ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
289	276	270	SER		SER	SER		SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
290	277	271	TRP		TRP	TRP		TRP	TRP	TRP		PHE	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
291	278	272	PHE		PHE	PHE		PHE	PHE	PHE		PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
292	279	273	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
293		274																			
294		275																			
295	280	276	ASP		ASP	ASP		ASN	ASN	ASN		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
296	281	277	ASN		ASN	ASN		ASN	ASN	ASN		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
297	278	278																			
298	279																				
299	282	280	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
300	283	281	GLU		GLU	GLU		GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
301	284	282	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
302	285	283	HIS		HIS	HIS		HIS	HIS	HIS		HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS
303	286		THR		THR	THR		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
304	287	284	ALA		ALA	ALA		ALA	ALA	ALA		ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
305	288	285	GLN		GLN	GLN		GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
306	289	286	THR		THR	THR		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
307	290	287	GLN		GLN	GLN		GLN	GLN	GLN		GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
308	291	288	PRO		PRO	PRO		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
309	292	289	ARG		ARG	ARG		HIS	HIS	HIS		HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS
310	293	290	GLU		GLU	GLU		ARG	ARG	ARG		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
311	294	291	GLU		GLU	GLU		GLU	GLU	GLU		GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
312	295	292	GLN		GLN	GLN		ASP	ASP	ASP		ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
313	296	293	PHE		PHE	PHE		TYR	TYR	TYR		TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
314	297	294	ASN		ASN	ASN		ASN	ASN	ASN		ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN
315	295	295																			
316	296	296																			
317	298	297	SER		SER	SER		SER	SER	SER		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER
318	299	298	THR		THR	THR		THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
319	300	299	PHE		PHE	PHE		ILE	ILE	ILE		ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
320	301	300	ARG		ARG	ARG		ARG	ARG	ARG		ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
321	302	301	SER		SER	SER		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
322	303	302	VAL		VAL	VAL		VAL	VAL	VAL		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
323	304	303	SER		SER																

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

EU INDEX	OU INDEX	100 MOPC 47A	101 MOPC 315	102 MOPC 511	103 MOPC 511	104 MOPC 511	105 MOPC 511	106 MOPC 511	107 MOPC 511	108 MOPC 511	109 MOPC 511	110 MOPC 511	111 MOPC 511	112 MOPC 511	113 MOPC 511	114 MOPC 511	115 MOPC 511	116 MOPC 511	117 MOPC 511	118 MOPC 511	119 MOPC 511	120 MOPC 511
243A																						
243B																						
243C																						
243D																						
243E																						
243F																						
243G																						
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243I																						
244	231																					
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251	238																					
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282	269																					
283	270																					
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338	325																					
339	326																					
340	327																					
341	328																					
342	329																					
343	330																					

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

EU INDEX	CU INDEX	140 IGG2	141 MOO	142 PIG IGG	143 SHEEP PSHC CL	144 HORSE IGG	145 BOVINE IGG	146 GOAT IGG	147 CHICKEN IGG CL	148 EGGS VR CL	149 REID CL	150 RE20 CL	151 Xenopus laevis CL	152 Xenopus laevis CL	153 Xenopus laevis c14(12) CL	154 Xenopus laevis c15(12) CL	155 Xenopus laevis c40(12) CL
243A																	
243B																	
243C																	
243D																	
243E																	
243F																	
243G	230		VAL						ILE	GLU	ASP		CYS	PRO			
243H	231		MET						PRO	ARG			GLN	VAL			
243I	232								THR	PRO	VAL		ASP	LYS			
244	231	PRO			PRO												
245	232	PRO			PRO												
245A																	
245B																	
245C																	
246	233	233	GLU	THR	GLU				PRO	LYS	VAL		PRO	VAL			
247	234	234	ASN	LEU	LEU				ASN	PRO	HIS		GLU	GLU			
248	235	235	GLY	PRO	PRO				GLY	PRO	HIS	PRO	PRO	LYS			
249	236	236	GLY	PRO	GLY				ILE	ARG	PRO	GLN	ILE	PRO			
250	237	237	GLY	GLU	GLY				LEU	PRO	VAL	PRO	PRO	VAL			
251	238	238	PRO	VAL	PRO												
251A																	
251B																	
252	239	239	SER	SER	SER				PHE	VAL	THR	GLN	THR	SER			
253	240	240	VAL	GLY	VAL				VAL	LEU	ILE	LEU	VAL	ILE			
254	241	241	PHE	PHE	PHE				THR	SER	THR	ILE	GLU	HIS			
255	242	242	ILE	ILE	ILE				MET	ILE	ILE	PRO	ILE	PRO			
256	243		PHE		PHE				HIS								
257	244	243	PRO	PRO	PRO				PRO	MET		LEU	LEU	PRO			
258	245	244	PRO	PRO	PRO				PRO	THR		VAL	GLN	SER			
259	246	245	LYS	ARG	LYS				SER	PRO	THR	PRO	GLY	LYS			
260	247	246	PRO	ASP	PRO				ARG	SER	ALA	SER	PRO	ASP			
261	248	247	LYS	ALA	PRO				GLU	GLN	LEU	PRO	CYS	ALA			
262	249	248	ASP	PHE	ASP				ASP	GLU	ASP	GLU	ALA	LEU			
263	250		THR		THR				PHE	GLU	GLY	THR	SER	ALA			
264	251	249	LEU	PHE	LEU				GLY	LEU	ILE	LEU	SER	LEU			
265	252	250	MET	GLY	THR				THR	LYS	HIS		LYS	ASN			
266	253	251	ILE	ASN	ILE				PRO	LEU	ARG	ASN	GLU	SER			
267	254	252	SER	PRO	SER				PHE	ASN	GLN	GLN	VAL	SER			
268	255	253	LEU	ARG	GLY				ARG	LYS	GLY	THR	GLU	LEU			
269	256	254	THR	LYS	THR				ASN	THR	LYS	THR	LEU	PHE			
270	257	255	PRO	GLU	PRO				ALA	ALA	ALA	ALA					
271	258	256	ARG	PRO	GLU				SER	THR	ILE	VAL					
272	259	257	VAL	LEU	VAL				ILE	PHE	ALA	LEU					
273	260	258	THR	ILE	THR				LEU	ALA	VAL	GLY	LEU	ILE			
274	261	259	CYS	CYS	CYS				CYS	CYS	CYS	CYS	CYS	CYS			
275	262	260	VAL	GLN	VAL				GLN	LEU	LEU	MET	LEU	LEU			
276	263	261	VAL	ALA	VAL				THR	ALA	VAL	ILE	ILE	ALA			
277	264	262	VAL	SER	VAL				ARG	THR	ASN	SER	THR	THR			
278	265	263	ASP	GLY	ASP				GLY	ASP	ASN	GLY	GLY	ASN			
279	266	264	VAL	PHE	VAL				ARG	PHE	PHE	PHE	TYR	PHE			
280	267	265	SER	SER	GLY				ARG	TYR	THR	SER	ALA	THR			
281	268	266	GLN	PRO	GLN				ARG	PRO	PRO	PRO	PRO	THR			
282	269	267	ASP	ARG	ASP					LYS	ALA	ASP	SER	PRO			
283	270	268	GLU	GLN	ASP				PRO	GLY	ILE	ASN	GLU	HIS			
284	271		PRO		PRO				THR	HIS	PHE	ILE	ILE	ILE			
285	272		GLU		GLU				GLU	SER	THR	LYS	LYS	VAL			
286	273	269	VAL	VAL	VAL				VAL	PHE	VAL	VAL	VAL	ILE			
287	274		GLN		GLN												
288	275		PHE		PHE												
289	276	270	THR	TRP	SER				THR	LYS	ASN	SER	HIS	LYS			
290	277	271	TRP	SER	TRP				TRP	TRP	TRP	TRP	TRP	TRP			
291	278	272	PHE	LEU	PHE				TYR	LEU	LEU	LYS	LEU	LEU			
292	279	273	VAL	ARG	VAL				LYS	ARG	LYS	LYS	LEU	LYS			
293		274	ASP		ASP				ASN	ASP	ASN	ALA	ASN	ASN			
294		275	GLY		GLY				GLY	GLY	GLY	GLY	GLY	GLY			
295	280	276	ASP	LYS	ASP				SER	LYS	LYS	LEU	GLN	ASN			
296	281	277	ASN	GLN	ASN				GLU	PRO	ASN	VAL	ASN	GLN			
297		278	ILE		ILE				VAL	VAL	LEU	GLN	THR	THR			
298		279	GLU		GLU				THR	ASP	ALA	ASN	THR	GLU			
299	282	280	LYS	SER	VAL				ASP	SER	GLY	ILE	ILE	GLU			
300	283	281	PRO	GLY	GLU					GLY	GLY	VAL	SER	GLY			
301	284	282	VAL	VAL	VAL					ILE	ILE	VAL	PRO	VAL			
302	285	283	GLY	THR	ARG					ALA	VAL	LEU	SER	ARG			
303	286		ASN		THR												
304	287	284	ALA	THR	ALA									ASN	VAL		
305	288	285	GLU	ASN	ARG					THR	THR	PRO	SER	GLU			
306	289	286	THR	GLU	THR				ALA	LEU	SER	SER	LYS	GLU			
307	290	287	LYS	VAL	LYS				ALA	THR	PRO	THR	PRO	PRO			
308	291	288	PRO	GLX	PRO				ALA	GLU	ALA	PRO	CYS	VAL			
309	292	289	ARG	ALA	ARG				ALA	CYS	PHE	ARG	LYS	GLU			
310	293	290	VAL	GLX	GLU				THR	GLN	GLN	THR	GLU	ASP			
311	294	291	GLU	ALA	GLU				THR	LYS	VAL	ASN	GLU	LYS			
312	295	292	GLN	LYS	GLN				ALA	LYS	ASN	GLY	ASN	LYS			
313	296	293	TYR	GLX	PHE				THR	GLY	GLY	GLY	GLY	ARG			
314	297	294	ASN	SER	ASN				THR				THR	GLY			
315		295	GLY						VAL	ASP	THR			PHE			
316		296	PRO						LYS	GLY				THR			
317	298	297	THR	THR	SER				PRO	SER	ASN		SER	ALA			
318	299	298	THR	THR	THR				GLU	PHE	PHE	PHE	ARG	THR			
319	300	299	PHE	TYR	PHE				VAL	THR	SER	GLU	SER	SER			
320	301	300	ARG	LYS	ARG				VAL	ALA	ALA	THR	LYS	TYR			
321	302	301	VAL	VAL	VAL				ALA	SER	THR	VAL	VAL	LEU			
322	303	302	GLU	THR	VAL				GLU	SER	SER	ALA	SER	SER			
323	304	303	SER	SER	SER				GLU	SER	PHE	TYR	VAL	ILE			
324	305	304	VAL	MET	ALA				ARG	LEU	LEU	LEU	PRO	THR			
325	306	305	LEU	LEU	LEU				ILE	GLN	THR	PRO	LYS	ARG			
326	307	306	PRO	THR	PRO				SER	ALA	PHE	LEU	GLU	LYS			
327	308	307	ILE	ILE	ILE				VAL	SER	THR	ASN	ASP	GLU			
328	309	308	GLN	GLN	GLN				THR	GLU	ALA	VAL	TRP	TRP			
329	310	309	HIS	GLU	HIS				GLU	SER	GLU	GLU	ASN	ASP			
330	311	310	GLN	GLN	GLN				SER	THR	TRP	TRP	SER	LEU			
331	312	311	ASP	ALA	ASP				GLU	THR	TRP	TRP	GLU	THR			
332	313	312	TRP	TRP	TRP				TRP	LYS	PHE	THR	ASP	ASP			
333	314	313	LEU	LEU	THR				ASP	ARG	GLY	ASN	SER	LEU			
334	315	314	ARG	SER	GLY												
335	316	315	GLY	GLN	GLY				THR	LEU			TYR	TYR			
336	317	316	LYS	SER	LYS				GLY	ASP	PHE	GLN	CYS	SER			
337	318	317	GLU	VAL	GLU				THR	THR	VAL	GLU	LYS	VAL			
338	319	318	PHE	PHE	PHE				PHE	PHE	TYR	TYR	VAL	VAL			
339	320	319	LYS	THR	LYS				SER	THR	THR	THR	THR	GLU			
340	321	320	CYS	CYS	CYS				CYS	CYS	CYS	CYS	HIS	HIS			
341	322	321	LYS	LYS	LYS				VAL	GLN	GLN	GLU	PRO	ALA			
342	323	322	VAL	VAL	VAL				VAL	PHE	VAL	VAL	ALA	GLU			
343	324	323	TYR	GLU	HIS				GLU	ILE	ASN	THR	SER	SER			
344	325	324	ASN	HIS	ASN				GLU	GLN	HIS	HIS	HIS	GLY			
345	32																

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

EU INDEX	OU INDEX	156 Xenopus laevis J2 (I) 'CL	157 Xenopus laevis J4 (III) 'CL	158 Xenopus laevis J6 (I) 'CL	159 Xenopus laevis J12 (IV) 'CL	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
243A						4	1	4 (VAL)	
243B						4	1	4 (PRO)	
243C						4	1	4 (SER)	
243D						4	1	5 (THR)	
243E						5	1	5 (PRO)	
243F						5	1	5 (PRO)	
243G	230					35	8	18 (VAL)	
243H	231					36	8	8 (VAL)	
243I	232					40	9	11 (+)	
244	231					63	6	37 (ALA)	10.
245	232					59	5	45 (PRO)	6.6
245A						9	2	5 (THR)	
245B						9	1	9 (PRO)	
245C						12	2	9 (PRO)	
246	233	233				91	10	44 (GLU), 41 (GLU)	21., 22.
247	234	234				95	12	48 (LEU)	24.
248	235	235				96	13	36 (LEU)	35.
249	236	236				96	8	43 (GLY)	19.
250	237	237				95	12	44 (GLY)	26.
251	238	238				94	6	54 (PRO)	10.
251A						12	1	12 (CYS)	
251B						12	2	8 (HIS)	
252	239	239				97	8	60 (SER)	13.
253	240	240				97	8	73 (VAL)	11.
254	241	241				96	11	62 (PHE)	17.
255	242	242				94	8	36 (ILE)	21.
256	243					76	6	47 (PHE)	9.7
257	244	243				94	8, 9	64 (PRO)	12., 13.
258	245	244				93	8	65 (PRO)	11.
259	246	245				94	10	41 (LYS)	23.
260	247	246				94	10, 11	35 (PRO)	27., 30.
261	248	247				96	10, 11	46 (LYS)	21., 23.
262	249	248				96	11	57 (ASP), 56 (ASP)	13., 14.
263	250					85	12	29 (THR)	35.
264	251	249				96	7	66 (LEU)	10.
265	252	250				97	11	41 (MET)	26.
266	253	251				103	10, 11	53 (ILE)	19., 21.
267	254	252				101	10	47 (SER)	21.
268	255	253				11	9	38 (ARG)	29.
269	256	254				99	9	57 (THR)	16.
270	257	255				97	5	48 (PRO)	10.
271	258	256				97	11	31 (GLU), 29 (GLU)	34., 37.
272	259	257				98	5	47 (VAL)	10.
273	260	258				98	9	65 (THR)	14.
274	261	259				98	1	98 (CYS)	1.
275	262	260				99	7	49 (VAL)	14.
276	263	261				97	5	59 (VAL)	8.2
277	264	262				97	7	50 (VAL)	14.
278	265	263				96	3	48 (ASP)	6.
279	266	264				96	8	42 (VAL)	18.
280	267	265				94	9	54 (SER)	16.
281	268	266				85	9	20 (+)	38.
282	269	267				84	9	27 (ASP)	28.
283	270	268				85	9	47 (ASP)	16.
284	271					82	9	51 (PRO)	14.
285	272					93	10	34 (GLU), 32 (GLU)	27., 29.
286	273	269				93	6	73 (VAL)	7.6
287	274					70	7, 8	36 (GLN), 34 (GLN)	14., 16.
288	275					75	6	48 (PHE)	9.4
289	276	270				94	8	30 (SER)	25.
290	277	271				93	4	79 (TRP)	4.7
291	278	272				94	8	28 (TYR)	27.
292	279	273				94	9	37 (VAL)	23.
293		274				22	5	10 (ASP)	11.
294		275				22	2	21 (GLY)	2.1
295	280	276				90	11	31 (ASP), 30 (ASP)	32., 33.
296	281	277				94	11	27 (ASN), 25 (ASN)	38., 41.
297		278				30	7	16 (VAL)	13.
298		279				22	8	7 (GLU)	25.
299	282	280				93	8, 9	35 (VAL)	21., 24.
300	283	281				91	10	33 (GLU), 32 (GLU)	28.
301	284	282				91	9	57 (VAL)	14.
302	285	283				91	13	30 (HIS)	39.
303	286					59	5	23 (THR)	13.
304	287	284				88	7	42 (ALA)	15.
305	288	285				91	12	22 (LYS)	50.
306	289	286				92	11	34 (THR)	30.
307	290	287				92	11	19 (+)	53.
308	291	288				91	11	24 (PRO)	42.
309	292	289				91	15	39 (ARG)	35.
310	293	290				91	8	51 (GLU), 46 (GLU)	14., 16.
311	294	291				91	11	28 (GLU), 26 (GLU)	36., 38.
312	295	292				91	12, 13	33 (GLN), 31 (GLN)	33., 38.
313	296	293				91	9, 10	26 (GLY)	31., 35.
314	297	294				87	9	40 (ASN), 34 (ASN)	20., 23.
315		295				32	8	12 (GLY)	21.
316		296				32	5	15 (PRO)	11.
317	298	297				75	10	39 (SER)	19.
318	299	298				76	6	56 (THR)	8.1
319	300	299				91	10	36 (TYR)	25.
320	301	300				90	8	39 (ARG)	18.
321	302	301				96	7	73 (VAL)	9.2
322	303	302				96	10	45 (VAL)	21.
323	304	303				95	6	90 (SER)	6.3
324	305	304				96	11	30 (VAL)	35.
325	306	305				96	7	90 (LEU)	7.5
326	307	306				97	10	41 (+)	24.
327	308	307				97	9	52 (ILE)	17.
328	309	308				97	12	15 (GLN), 14 (GLN)	78., 83.
329	310	309				97	8	46 (HIS)	17.
330	311	310				96	8	49 (GLN), 46 (GLN)	16., 17.
331	312	311				94	11	53 (ASP), 51 (ASP)	20.
332	313	312				95	5	90 (TRP)	5.3
333	314	313				95	9	54 (LEU)	16.
334	315	314				94	11	35 (SER)	30.
335	316	315				96	9	63 (GLY)	14.
336	317	316				98	11	51 (LYS)	21.
337	318	317				93	8	42 (GLU)	18.
338	319	318				93	3	56 (PHE)	5.
339	320	319				92	5	46 (LYS)	10.
340	321	320				92	2	90 (CYS)	2.
341	322	321				92	8	48 (LYS)	15.
342	323	322				92	5	77 (VAL)	6.
343	324	323				93	9	20 (+)	42.
344	325	324				92	7	35 (ASN)	18.
345	326	325				93	9	35 (LYS)	24.
346	327	326				94	9	34 (GLY)	25.
347	328	327				94	12	61 (LEU)	18.
348	329	328				94	10	46 (PRO)	20.
349	330	329				94	8	31 (ALA)	24.
350	331	330				87	8	49 (PRO)	16.
351	332	331				79	7	44 (ILE)	13.
351A						3	3	1 (+)	
352	333	332				95	10	41 (GLU)	23.
353	334	333				96	10	37 (LYS)	26.
354	335	334				95	9	66 (THR)	13.
355	336	335				96	7	56 (ILE)	12.
356		336				34	6	10 (MET)	20.
357	337	337				95	8	48 (SER)	16.
358	338	338				96	12	58 (LYS)	20.
359	339	339				74	8	23 (ALA)	26.
360	340					61	7	34 (LYS)	13.

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